

SEQUENCE LISTING

<110> Boehringer Ingelheim Pharma KG

<120> Method for identifying substances which positively influence inflammatory conditions of chronic inflammatory airway diseases

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<150> UK 0021484.1

<151> 2000-09-01

<160> 24

<170> PatentIn Ver. 2.1

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<211> 1910

<212> DNA

<213> Homo sapiens

<400> 1

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 Phe Ser Lys Glu Glu Gly Asp Trp Asn Ser Ser Lys Tyr Asn Cys Ser
 50 55 60
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 65 70 75 80
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 Lys Ser Phe Gly Met Arg Gly Ser Glu Gly Cys Ala Tyr Leu Ser Asp
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Asp Leu Ile Ala Ile Val Ala Gly Leu Val Gln Thr Val Leu Tyr Cys
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ctctgtccac attaaactaa cagcattaat gc 3992

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<210> 10
 <211> 972
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Gly Pro Gly Val Leu Leu Leu Leu Leu Val Ala Thr Ala Trp His
 1 5 10 15
 Gly Gln Gly Ile Pro Val Ile Glu Pro Ser Val Pro Glu Leu Val Val
 20 25 30
 Lys Pro Gly Ala Thr Val Thr Leu Arg Cys Val Gly Asn Gly Ser Val
 35 40 45
 Glu Trp Asp Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly
 50 55 60
 Ser Ser Ser Ile Leu Ser Thr Asn Asn Ala Thr Phe Gln Asn Thr Gly

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370	375	380
Asn Pro Gly Gly Trp Arg Ala Leu Thr Phe Glu Leu Thr Leu Arg Tyr		
385	390	395 400
Pro Pro Glu Val Ser Val Ile Trp Thr Phe Ile Asn Gly Ser Gly Thr		
	405	410 415
Leu Leu Cys Ala Ala Ser Gly Tyr Pro Gln Pro Asn Val Thr Trp Leu		
	420	425 430
Gln Cys Ser Gly His Thr Asp Arg Cys Asp Glu Ala Gln Val Leu Gln		
	435	440 445
Val Trp Asp Asp Pro Tyr Pro Glu Val Leu Ser Gln Glu Pro Phe His		
	450	455 460
Lys Val Thr Val Gln Ser Leu Leu Thr Val Glu Thr Leu Glu His Asn		
	465	470 475 480
Gln Thr Tyr Glu Cys Arg Ala His Asn Ser Val Gly Ser Gly Ser Trp		
	485	490 495
Ala Phe Ile Pro Ile Ser Ala Gly Ala His Thr His Pro Pro Asp Glu		
	500	505 510
Phe Leu Phe Thr Pro Val Val Val Ala Cys Met Ser Ile Met Ala Leu		
	515	520 525
Leu Leu Leu Leu Leu Leu Leu Leu Leu Tyr Lys Tyr Lys Gln Lys Pro		
	530	535 540
Lys Tyr Gln Val Arg Trp Lys Ile Ile Glu Ser Tyr Glu Gly Asn Ser		
	545	550 555 560
Tyr Thr Phe Ile Asp Pro Thr Gln Leu Pro Tyr Asn Glu Lys Trp Glu		
	565	570 575
Phe Pro Arg Asn Asn Leu Gln Phe Gly Lys Thr Leu Gly Ala Gly Ala		
	580	585 590
Phe Gly Lys Val Val Glu Ala Thr Ala Phe Gly Leu Gly Lys Glu Asp		
	595	600 605
Ala Val Leu Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala His Ala		
	610	615 620
Asp Glu Lys Glu Ala Leu Met Ser Glu Leu Lys Ile Met Ser His Leu		
	625	630 635 640
Gly Gln His Glu Asn Ile Val Asn Leu Leu Gly Ala Cys Thr His Gly		
	645	650 655
Gly Pro Val Leu Val Ile Thr Glu Tyr Cys Cys Tyr Gly Asp Leu Leu		
	660	665 670
Asn Phe Leu Arg Arg Lys Ala Glu Ala Met Leu Gly Pro Ser Leu Ser		

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675					680					685					
Pro	Gly	Gln	Asp	Pro	Glu	Gly	Gly	Val	Asp	Tyr	Lys	Asn	Ile	His	Leu
690					695					700					
Glu	Lys	Lys	Tyr	Val	Arg	Arg	Asp	Ser	Gly	Phe	Ser	Ser	Gln	Gly	Val
705					710					715					720
Asp	Thr	Tyr	Val	Glu	Met	Arg	Pro	Val	Ser	Thr	Ser	Ser	Asn	Asp	Ser
				725					730					735	
Phe	Ser	Glu	Gln	Asp	Leu	Asp	Lys	Glu	Asp	Gly	Arg	Pro	Leu	Glu	Leu
			740					745					750		
Arg	Asp	Leu	Leu	His	Phe	Ser	Ser	Gln	Val	Ala	Gln	Gly	Met	Ala	Phe
		755					760					765			
Leu	Ala	Ser	Lys	Asn	Cys	Ile	His	Arg	Asp	Val	Ala	Ala	Arg	Asn	Val
						775					780				
Leu	Leu	Thr	Asn	Gly	His	Val	Ala	Lys	Ile	Gly	Asp	Phe	Gly	Leu	Ala
785						790					795				800
Arg	Asp	Ile	Met	Asn	Asp	Ser	Asn	Tyr	Ile	Val	Lys	Gly	Asn	Ala	Arg
				805					810					815	
Leu	Pro	Val	Lys	Trp	Met	Ala	Pro	Glu	Ser	Ile	Phe	Asp	Cys	Val	Tyr
			820					825					830		
Thr	Val	Gln	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Ile	Leu	Leu	Trp	Glu	Ile
			835				840						845		
Phe	Ser	Leu	Gly	Leu	Asn	Pro	Tyr	Pro	Gly	Ile	Leu	Val	Asn	Ser	Lys
			850			855					860				
Phe	Tyr	Lys	Leu	Val	Lys	Asp	Gly	Tyr	Gln	Met	Ala	Gln	Pro	Ala	Phe
865						870					875				880
Ala	Pro	Lys	Asn	Ile	Tyr	Ser	Ile	Met	Gln	Ala	Cys	Trp	Ala	Leu	Glu
			885						890					895	
Pro	Thr	His	Arg	Pro	Thr	Phe	Gln	Gln	Ile	Cys	Ser	Phe	Leu	Gln	Glu
			900					905					910		
Gln	Ala	Gln	Glu	Asp	Arg	Arg	Glu	Arg	Asp	Tyr	Thr	Asn	Leu	Pro	Ser
			915				920					925			
Ser	Ser	Arg	Ser	Gly	Gly	Ser	Gly	Ser	Ser	Ser	Ser	Glu	Leu	Glu	Glu
			930			935					940				
Glu	Ser	Ser	Ser	Glu	His	Leu	Thr	Cys	Cys	Glu	Gln	Gly	Asp	Ile	Ala
945						950					955				960
Gln	Pro	Leu	Leu	Gln	Pro	Asn	Asn	Tyr	Gln	Phe	Cys				
				965					970						

<210> 11
 <211> 1696
 <212> DNA
 <213> Homo sapiens

<400> 11
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 gggctgagtc tgggccccag gaccacagtg caggcagggc acctcccaa gcccaccctc 180
 tgggctgagc caggctctgt gatcatccag ggaagtccctg tgacctcag gtgtcagggg 240
 agccttcagg ctgaggagta ccatctatat agggaaaaca aatcagcatc ctgggttaga 300
 cggatacaag agcctgggaa gaatggccag ttcccatcc catccatcac ctgggaacac 360
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 ctggagctgg tggtagacagg agcctacagc aaaccacccc tctcagctct gcccagccct 480
 gtggtagacct taggagggaa cgtgaccctc cagtgtgtct cacagggtggc atttgacggc 540
 ttcatctctgt gtaagggaag agaagatgaa caccacaac gcctgaactc ccattcccat 600
 gcccgtgggt ggctcctgggc catcttctcc gtgggccccg tgagcccagag tcgcagggtgg 660
 tcgtacaggt gctatgctta tgactcgaac tctccctatg tgtggtctct acccagtgat 720
 ctcttgagc tcctgggtccc aggtgtttct aagaagccat cactctcagt gcagccaggt 780
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 cagtacagat gctacagtgc acacaacctc tcctccgagt ggtcggcccc cagtgacccc 1020
 ctggacatcc tgatcacagg acagttctat gacagaccct ctctctcggg gcagccgggtc 1080
 cccacagtag cccagggaaa gaacgtgacc ctgctgtgtc agtcacgggg gcagttccac 1140
 actttccttc tgaccaagga gggggcaggg catccccac tgcatctgag atcagagcac 1200
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 cccctggagc tcgtggtctc agcatcccta ggccaacacc cccaggatta cacagtggag 1380
 aatctcatcc gcatgggtgt ggctggcttg gtccctgggtg tcctcgggat tctgctatct 1440
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 acaatgcata ctccagcgtg gtggagcctc agggacagat ctgatgatcc caggaggctc 1560
 tggaggacaa tctaggacct acattatctg gactgtatgc tggtcatttc tagagacagc 1620
 aatcaatatt tgagtgtgaa gaaactgtct ggggtgattc ctagaagatc attaaactgt 1680
 ggtacatctt tttgtc 1696

<210> 12
 <211> 466
 <212> PRT
 <213> Homo sapiens

<400> 12
 Met Thr Pro Ile Leu Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly
 1 5 10 15
 Pro Arg Thr His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp
 20 25 30
 Ala Glu Pro Gly Ser Val Ile Ile Gln Gly Ser Pro Val Thr Leu Arg
 35 40 45
 Cys Gln Gly Ser Leu Gln Ala Glu Glu Tyr His Leu Tyr Arg Glu Asn
 50 55 60
 Lys Ser Ala Ser Trp Val Arg Arg Ile Gln Glu Pro Gly Lys Asn Gly
 65 70 75 80

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Gln	Phe	Pro	Ile	Pro	Ser	Ile	Thr	Trp	Glu	His	Ala	Gly	Arg	Tyr	His	
				85					90					95		
Cys	Gln	Tyr	Tyr	Ser	His	Asn	His	Ser	Ser	Glu	Tyr	Ser	Asp	Pro	Leu	
			100					105					110			
Glu	Leu	Val	Val	Thr	Gly	Ala	Tyr	Ser	Lys	Pro	Thr	Leu	Ser	Ala	Leu	
		115					120					125				
Pro	Ser	Pro	Val	Val	Thr	Leu	Gly	Gly	Asn	Val	Thr	Leu	Gln	Cys	Val	
	130					135					140					
Ser	Gln	Val	Ala	Phe	Asp	Gly	Phe	Ile	Leu	Cys	Lys	Glu	Gly	Glu	Asp	
145					150					155					160	
Glu	His	Pro	Gln	Arg	Leu	Asn	Ser	His	Ser	His	Ala	Arg	Gly	Trp	Ser	
				165					170					175		
Trp	Ala	Ile	Phe	Ser	Val	Gly	Pro	Val	Ser	Pro	Ser	Arg	Arg	Trp	Ser	
			180					185					190			
Tyr	Arg	Cys	Tyr	Ala	Tyr	Asp	Ser	Asn	Ser	Pro	Tyr	Val	Trp	Ser	Leu	
		195					200					205				
Pro	Ser	Asp	Leu	Leu	Glu	Leu	Leu	Val	Pro	Gly	Val	Ser	Lys	Lys	Pro	
	210					215					220					
Ser	Leu	Ser	Val	Gln	Pro	Gly	Pro	Met	Val	Ala	Pro	Gly	Glu	Ser	Leu	
225					230					235					240	
Thr	Leu	Gln	Cys	Val	Ser	Asp	Val	Gly	Tyr	Asp	Arg	Phe	Val	Leu	Tyr	
				245				250						255		
Lys	Glu	Gly	Glu	Arg	Asp	Phe	Leu	Gln	Arg	Pro	Gly	Trp	Gln	Pro	Gln	
			260					265					270			
Ala	Gly	Leu	Ser	Gln	Ala	Asn	Phe	Thr	Leu	Gly	Pro	Val	Ser	Pro	Ser	
		275					280					285				
His	Gly	Gly	Gln	Tyr	Arg	Cys	Tyr	Ser	Ala	His	Asn	Leu	Ser	Ser	Glu	
	290					295					300					
Trp	Ser	Ala	Pro	Ser	Asp	Pro	Leu	Asp	Ile	Leu	Ile	Thr	Gly	Gln	Phe	
305					310					315					320	
Tyr	Asp	Arg	Pro	Ser	Leu	Ser	Val	Gln	Pro	Val	Pro	Thr	Val	Ala	Pro	
				325					330					335		
Gly	Lys	Asn	Val	Thr	Leu	Leu	Cys	Gln	Ser	Arg	Gly	Gln	Phe	His	Thr	
			340					345					350			
Phe	Leu	Leu	Thr	Lys	Glu	Gly	Ala	Gly	His	Pro	Pro	Leu	His	Leu	Arg	
		355					360					365				
Ser	Glu	His	Gln	Ala	Gln	Gln	Asn	Gln	Ala	Glu	Phe	Arg	Met	Gly	Pro	
	370					375					380					

Val Thr Ser Ala His Val Gly Thr Tyr Arg Cys Tyr Ser Ser Leu Ser
385 390 395 400

Ser Asn Pro Tyr Leu Leu Ser Leu Pro Ser Asp Pro Leu Glu Leu Val
405 410 415

Val Ser Ala Ser Leu Gly Gln His Pro Gln Asp Tyr Thr Val Glu Asn
420 425 430

Leu Ile Arg Met Gly Val Ala Gly Leu Val Leu Val Val Leu Gly Ile
435 440 445

Leu Leu Phe Glu Ala Gln His Ser Gln Arg Ser Leu Gln Asp Ala Ala
450 455 460

Gly Arg
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<210> 13
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 13
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ttt 63

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 14
gtcgtcaaga tgctaccgtt cagga 25

<210> 15
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
ggggacaagt ttgtacaaaa aagcaggcta tggaaaccaa cttctcca 48

<210> 16
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
ggggaccact ttgtacaaga aagctgggtt cacattgcct gtaactcagt ctc 53

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
agcccatagc agatggcaac 20

<210> 18
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
tgtactttca actttgcatc ctgg 24

<210> 19
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
aagccaatga caaaccggat aatccctc 28

<210> 20
<211> 2051
<212> DNA
<213> Homo sapiens

<400> 20
cgccactttg ctggagcatt cactaggcga ggcgctccat cggactcact agccgcactc 60
atgaatcggc accatctgca ggatcacttt ctggaaatag acaagaagaa ctgctgtgtg 120
ttccgagatg acttcattgc caaggtgttg ccgccggtgt tggggctgga gtttatcttt 180


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gggcttcttg gcaatggcct tgccctgtgg attttctgtt tccacctcaa gtccctggaaa 240
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ccgttcgtga tggactacta tgtgcgcggt tcagactgga actttgggga catcccttgc 360
cggttggtgc tcttcatgtt tgccatgaac cgccagggca gcatcatctt cctcacgggtg 420
gtggcggtag acaggatatt ccgggtgggt catccccacc acgccctgaa caagatctcc 480
aattggacag cagccatcat ctcttgccct ctgtggggca tcaactgttg cctaacagtc 540
cacctcctga agaagaagt gctgatccag aatggccctg caaatgtgtg catcagcttc 600
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gaccggcatg ccaagatcaa gagagccatc accttcatca tgggtgggtgc catcgtcttt 780
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attaaaaggg aaacgtgcct ctgccccacg ggtagagggg gtgcacgttc ctcttggttc 1980
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caaaaaaaaa a 2051

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<210> 21
 <211> 387
 <212> PRT
 <213> Homo sapiens

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<400> 21
Met Asn Arg His His Leu Gln Asp His Phe Leu Glu Ile Asp Lys Lys
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Asn Cys Cys Val Phe Arg Asp Asp Phe Ile Ala Lys Val Leu Pro Pro
      20              25              30

Val Leu Gly Leu Glu Phe Ile Phe Gly Leu Leu Gly Asn Gly Leu Ala
    35              40              45

Leu Trp Ile Phe Cys Phe His Leu Lys Ser Trp Lys Ser Ser Arg Ile
    50              55              60

Phe Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Ile Ile Cys Leu
    65              70              75              80

Pro Phe Val Met Asp Tyr Tyr Val Arg Arg Ser Asp Trp Asn Phe Gly
      85              90              95

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Asp	Ile	Pro	Cys	Arg	Leu	Val	Leu	Phe	Met	Phe	Ala	Met	Asn	Arg	Gln	
			100					105					110			
Gly	Ser	Ile	Ile	Phe	Leu	Thr	Val	Val	Ala	Val	Asp	Arg	Tyr	Phe	Arg	
		115					120					125				
Val	Val	His	Pro	His	His	Ala	Leu	Asn	Lys	Ile	Ser	Asn	Trp	Thr	Ala	
		130				135					140					
Ala	Ile	Ile	Ser	Cys	Leu	Leu	Trp	Gly	Ile	Thr	Val	Gly	Leu	Thr	Val	
145					150					155					160	
His	Leu	Leu	Lys	Lys	Lys	Leu	Leu	Ile	Gln	Asn	Gly	Pro	Ala	Asn	Val	
			165					170						175		
Cys	Ile	Ser	Phe	Ser	Ile	Cys	His	Thr	Phe	Arg	Trp	His	Glu	Ala	Met	
			180					185					190			
Phe	Leu	Leu	Glu	Phe	Leu	Leu	Pro	Leu	Gly	Ile	Ile	Leu	Phe	Cys	Ser	
		195					200					205				
Ala	Arg	Ile	Ile	Trp	Ser	Leu	Arg	Gln	Arg	Gln	Met	Asp	Arg	His	Ala	
		210				215					220					
Lys	Ile	Lys	Arg	Ala	Ile	Thr	Phe	Ile	Met	Val	Val	Ala	Ile	Val	Phe	
225					230					235					240	
Val	Ile	Cys	Phe	Leu	Pro	Ser	Val	Val	Val	Arg	Ile	Arg	Ile	Phe	Trp	
			245					250						255		
Leu	Leu	His	Thr	Ser	Gly	Thr	Gln	Asn	Cys	Glu	Val	Tyr	Arg	Ser	Val	
		260					265						270			
Asp	Leu	Ala	Phe	Phe	Ile	Thr	Leu	Ser	Phe	Thr	Tyr	Met	Asn	Ser	Met	
		275					280					285				
Leu	Asp	Pro	Val	Val	Tyr	Tyr	Phe	Ser	Ser	Pro	Ser	Phe	Pro	Asn	Phe	
		290				295					300					
Phe	Ser	Thr	Leu	Ile	Asn	Arg	Cys	Leu	Gln	Arg	Lys	Met	Thr	Gly	Glu	
305					310					315					320	
Pro	Asp	Asn	Asn	Arg	Ser	Thr	Ser	Val	Glu	Leu	Thr	Gly	Asp	Pro	Asn	
			325					330					335			
Lys	Thr	Arg	Gly	Ala	Pro	Glu	Ala	Leu	Met	Ala	Asn	Ser	Gly	Glu	Pro	
			340				345						350			
Trp	Ser	Pro	Ser	Tyr	Leu	Gly	Pro	Thr	Ser	Asn	Asn	His	Ser	Lys	Lys	
		355					360					365				
Gly	His	Cys	His	Gln	Glu	Pro	Ala	Ser	Leu	Glu	Lys	Gln	Leu	Gly	Cys	
		370				375					380					
Cys	Ile	Glu														
385																

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 22
agcccatagc agatggcaac 20

<210> 23
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
tgtactttca actttgcatc ctgg 24

<210> 24
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
aagccaatga caaaccggat aatccctc 28

094460
408460
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